

# FIGURE 1

TABLE 1

Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

| Exon Number | Exon length(bp) | CDNA position | splice acceptor | flanking exon sequence           | splice donor | Intron number | Intron Size approximate (Kb) |
|-------------|-----------------|---------------|-----------------|----------------------------------|--------------|---------------|------------------------------|
| 1           | 55              | 1-55          |                 | ...CTG CAC G<br>L H              | GTAAGGCCAC   | 1             | 0.3                          |
| 2           | 140             | 56-195        | TCTCCTTAAG      | TG TCC.....GAC GTG<br>V S D V    | GTGAGTCCCG   | 2             | Unknown                      |
| 3           | 45              | 196-240       | TTTTTGAG        | GAT GAG.....CAA ATG<br>D E Q M   | GTAAGTTAAG   | 3             | 9.0                          |
| 4           | 110             | 241-350       | TGTGTGTCAG      | TCT TGG.....AAC AG<br>S W N S    | GTAAGCATAT   | 4             | Unknown                      |
| 5           | 80              | 351-430       | CTGTTTCTAG T    | GCT GAT.....CCT CCA G<br>A D P P | GTAAGCTGCA   | 5             | 4.0                          |
| 6           | 168             | 431-598       | ACCCACACAG      | GC ATA.....CTA GTG G<br>G I L V  | GTAAGCCATG   | 6             | 1.0                          |
| 7           | 195             | 599-793       | CCCTATGGAG      | GA ATC.....TCC CTG G<br>G I S L  | GTAAGCGCCC   | 7             | 1.0                          |
| 8           | 87              | 794-880       | TATGTTTAG       | GG ATA.....TTG ATA G<br>G I L I  | GTAAGGCAAG   | 8             | 3.5                          |
| 9           | 110             | 881-990       | CTCTCCACAG      | CC CAG.....AAG TGG<br>A Q K W    | GTACGTTCT    | 9             | 5.0                          |
| 10          | 519             | 991-1509      | GTCTCCCCAG      | ACC AGA...<br>T R                |              |               |                              |

TABLE 2  
Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

| DNA             | EXONS<br>CONT. | EXON 6<br>+/- 497-498 | EXON 7<br>654 | EXON 7<br>690 | EXON 10<br>1269 | EXON 10<br>1335 | EXON 10<br>176630 |
|-----------------|----------------|-----------------------|---------------|---------------|-----------------|-----------------|-------------------|
| CHR15<br>HYBRID | 5-10<br>1-10   | +TG<br>-TG            | C/T           | G/A           | C/C             | C/C             | 6GT<br>8GT        |
| YAC             |                |                       |               |               |                 |                 |                   |
| D-948a10        | 5-10           | -TG                   | T             | A             | C               | C               | 6GT               |
| D-853b12        | 6-10           | -TG                   | T             | A             | C               | C               | 6GT               |
| D/F             | 5-10           | +TG<br>-TG            | C/T           | G/A           | C/T             | C/C             | 6GT<br>8GT        |
| 969b11          | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-134h10        | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-776a12        | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-791e6         | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-811b6         | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-953g6         | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-859c11        | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-810f11        | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| F-801e1         | 1-10           | +TG                   | C             | G             | C               | C               | 6GT<br>8GT        |
| BAC             |                |                       |               |               |                 |                 |                   |
| F-467o18        | 1-10           | +TG                   | C             | G             | C               | T               | 8GT               |

| DNA                       | Control<br># | EXON 6<br>+/- 497-498 | EXON 7<br>654 | EXON 7<br>690  | EXON 10<br>1269 | EXON 10<br>1335 |               |                |          |          |                 |               |
|---------------------------|--------------|-----------------------|---------------|----------------|-----------------|-----------------|---------------|----------------|----------|----------|-----------------|---------------|
| Control<br>Genomic<br>DNA | 43           | +/<br>10              | -/-<br>33     | C/C<br>5<br>38 | T/T<br>0<br>0   | G/G<br>0<br>43  | A/A<br>0<br>0 | C/C<br>6<br>36 | C/T<br>1 | T/T<br>1 | C/C<br>24<br>19 | T/T<br>0<br>0 |

## FIGURE 3

TABLE 3  
Expression Analysis of Sequence Variants

| Bases 497-498 |     |           | Base 654  |     |           | Base 690  |     |           | Base 933  |     |           | Base 1296 |     |           | Base 1335 |     |           |           |
|---------------|-----|-----------|-----------|-----|-----------|-----------|-----|-----------|-----------|-----|-----------|-----------|-----|-----------|-----------|-----|-----------|-----------|
| Subj          | DNA | 1-10 cDNA | 5-10 cDNA |
| SL061         | +-  | +         | +-        | CT  | C         | CT        | GA  | G         | GA        | G   | G         | G         | CT  | CT        | CT        | C   | C         | C         |
| SL084         | +   | +         | +         | C   | C         | C         | GA  | G         | GA        | G   | G         | G         | CT  | C         | CT        | C   | C         | C         |
| SL111         | +-  | +         | +-        | CT  | C         | CT        | GA  | G         | GA        | G   | G         | G         | CT  | CT        | CT        | CT  | CT        | CT        |
| SL097         | +   | +         | +         | CT  | C         | CT        | GA  | G         | GA        | G   | G         | G         | CT  | C         | CT        | C   | C         | C         |
| SL089         | +   | +         | +         | C   | C         | C         | GA  | GA        | GA        | GA  | GA        | GA        | CT  | CT        | CT        | C   | C         | C         |
| SHSY          | +-  | +         | +-        | CT  | C         | CT        | GA  | GA        | GA        | GA  | GA        | GA        | C   | C         | C         | C   | C         | C         |

**FIGURE 4**

-392 agaacgcgcaag ggagagggtag agcctggcct tggcagccc ctggctggc cagaggcgcg aggccgagag  
 AP-2  
 -322 cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc gggagtacct cccgctcaca  
 -252 cctcgggctg cagttccctg ggtggccgccc gagacgctgg cccgggctgg agggatggcg gggcggggac  
 -182 gggggcgggg gcggggctcg tcacgtggag aggcgccgccc gggcgccgccc ggccggggcg cgccgcggc  
 CREB Sp1  
 -112 tccttaaagg cgcgcgagcc gagcggcgag gtgcctctgt gcccgcaggc gcaggccccgg gcgacagccg  
 -42 agacgtggag cgcgcggct cgctgcagct ccgggactca acATGCGCTG CTCGCCGGGA GGCCTCTGGC  
 Met  
 +29 TGGCGCTGGC CGCGTCGCTC CTGCACGgt aagccac

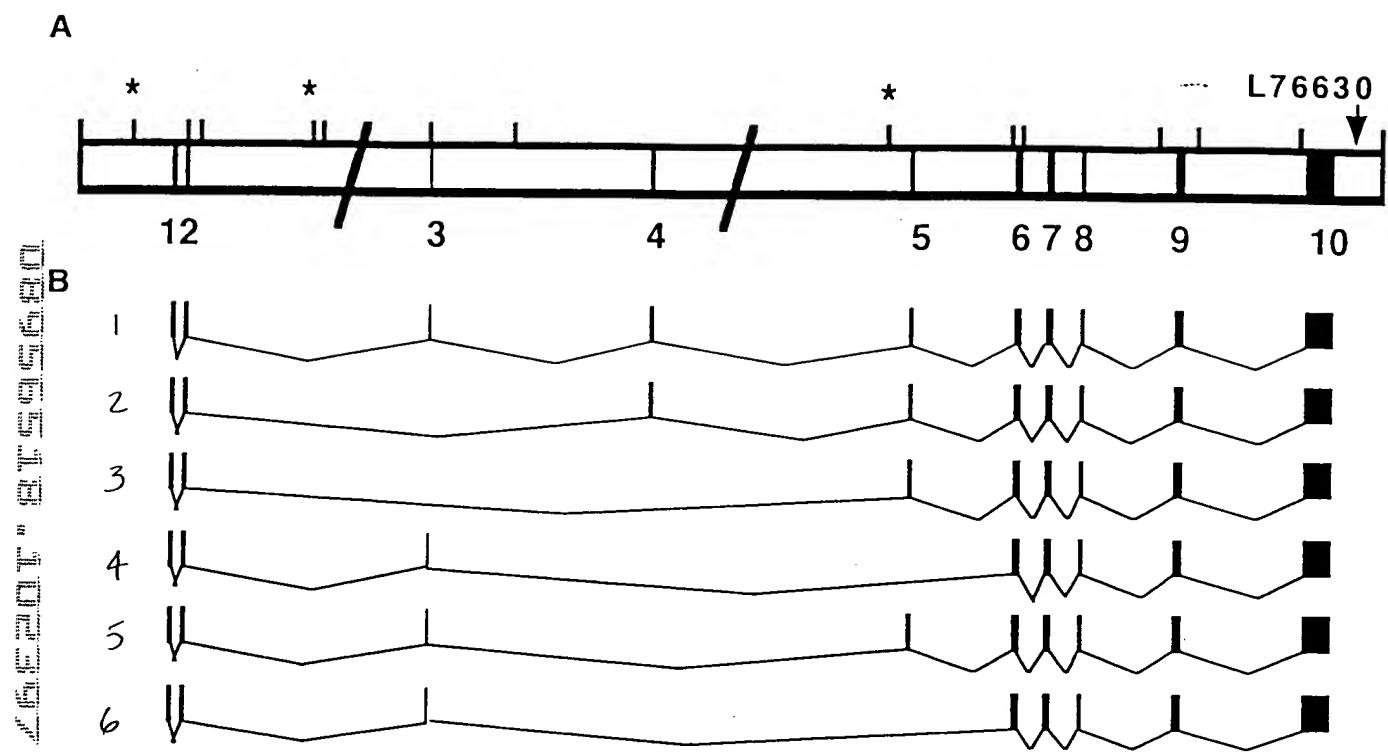
**FIGURE 5**

|        |            | CENTROMERE       |  | TELOMERE |  |
|--------|------------|------------------|--|----------|--|
|        |            | ALPHA-7 SEQUENCE |  |          |  |
|        |            | ALPHA-7 SEQUENCE |  |          |  |
| PAC    | SIZE<br>kb |                  |  |          |  |
| PAC    |            |                  |  |          |  |
| 64a1   | 1          |                  |  |          |  |
| 25919  |            |                  |  |          |  |
| BAC    |            |                  |  |          |  |
| 467018 |            |                  |  |          |  |
| YAC    |            |                  |  |          |  |
| 948a10 | 1730       |                  |  |          |  |
| 853b12 | 790        |                  |  |          |  |
| 895f6  | 1580       |                  |  |          |  |
| 969b11 | 1030       |                  |  |          |  |
| 776a12 | 1640       |                  |  |          |  |
| 791a6  | 1170       |                  |  |          |  |
| 811b6  | 1060       |                  |  |          |  |
| 953g6  | 1720       |                  |  |          |  |
| 134h10 | N.A.       |                  |  |          |  |
| 859c11 | 1330       |                  |  |          |  |
| 810f11 | 940        |                  |  |          |  |
| 801e1  | 1630       |                  |  |          |  |
| 966a4  | 1500       |                  |  |          |  |
| 764f8  | 740        |                  |  |          |  |
| 822g2  | 1280       |                  |  |          |  |

## FIGURE 6

|               |             |             |             |                     |             |             |             |
|---------------|-------------|-------------|-------------|---------------------|-------------|-------------|-------------|
|               |             |             |             |                     |             |             |             |
| <b>EXON D</b> |             |             |             |                     |             |             |             |
| 297bp         | CAGGCCGCCA  | CATAGCTCCC  | GCCAAGTCCT  | CGGTGCCCT           | TGCCATTTC   | CAGCCCGTTC  | CCACGAGGGT  |
|               | CACGGCGGGCG | GGGAGAGGTG  | GAGCCGCGAG  | AGCTCGGCCG          | GGGGCCCCGC  | CTGGTGGCCG  | CGGCCATGAC  |
|               | ACCGGCTCGG  | GAATGGCTCC  | TTTTCCGCGC  | CCCTCCCCGC          | GGAGGTGAGG  | GGAAGATGTC  | CATGTCAGGG  |
|               | TTCAAGGCCA  | AACCGAAGTT  | ACTGGCCTCT  | ATCTTCCAGG          | AGAACCCAGGA | GCCACAGCCG  | CGGCTCACGC  |
|               | CCCACCGCAA  | CATTAAGgtg  | agtcgc..... |                     |             |             |             |
|               |             | 297         |             |                     |             |             |             |
|               |             | 298         |             |                     |             |             |             |
| <b>EXON C</b> | ....ctc     | atttcagATT  | ACAAGTGGAC  | ACCTGAGTCA          | GCAGGACCTG  | GAATCCCAGA  | TGAGAGAGCT  |
| 125bp         | TATCTACACG  | ACTCAGATCT  | TGTTGTCACC  | CCCATTATTG          | ACAATCCAAA  | GGTGCAGAAA  | GCACTCTGAC  |
|               | AAgtgagttg  | ta.....     |             |                     |             |             |             |
|               | 422         |             | 423         |                     |             |             |             |
| <b>EXON B</b> | ..ttaaccac  | agATAATGAA  | ACAACCACCA  | TCGGTTAAAT          | TTGATGCAAA  | AATATTGCAT  | CTACCAGCAT  |
| 64bp          | TTTCAGgtag  | gatcat..... |             |                     |             |             |             |
|               | 486         |             | 487         |                     |             |             |             |
| <b>EXON A</b> | .....ttta   | ttcttagTTCC | AATTGCTAAT  | CCAGCATTG           | TGGATAGCTG  | CAAAC TGCAG | TATgtaaagta |
| 47bp          | aca.....    |             |             |                     |             |             | 533         |
|               |             | 534         |             |                     |             |             |             |
| <b>EXON 5</b> | ...ctgtttc  | tagTGCTGAT  | GAGCGCTTG   | ACGCCACATT          | CCACACTAAC  | GTGTTGGTGA  | ATTCTTCTGG  |
| 80bp          | GCATTGCCAG  |             | TACCTGCCTC  | CAGgtaaagctgca..... |             |             |             |
|               |             | 614         |             |                     |             |             |             |
| <b>EXON 6</b> | ....acccaca | cagGCATATT  | CAAGAGTTCC  | TGCTACATCG          |             |             |             |
| 27bp          |             |             |             | 640                 |             |             |             |

**FIGURE 7**



## FIGURE 8

1 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg  
61 aggccgagag cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc  
121 gggagtacct cccgctcaca cctcgggctg cagttccctg ggtggccgccc gagacgctgg  
181 cccgggctgg agggatggcg gggcggggac gggggcgggg gcggggctcg tcacgtggag  
241 aggcgcgcgg gggcgggcgg ggcggggcgg cgcgcggcgc tcctaaagg cgcgcgagcc  
301 gagcggcgag gtgcctctgt ggccgcaggc gcaggcccgg gcgacagccg agacgtggag  
361 cgcgccggct cgctgcagct ccgggactca ac

## FIGURE 9

1 agcccttcc caggcggtag cgggggcagt ggtgctgttgc ccctttaaa ctgcggcttg  
61 acgggagccg cgccctctgt cggtgagtc ggttataaag ggagcagccc cgccaggccgc  
121 cacatagctc ccgccaagtc ctcggtgccc ctggccattt tccagccgcg ctcccacgag  
181 ggtcacggcg ggggggagag gtggagccgc gagagctcgcc cgggggccgc cgccctgggtgg  
241 ccgcggccat gacagcggct cgggactggc tcctttccgc cggccctccc gccggaggtg  
301 aggggaagat gtccatgtca ggggtcaagg ccaaaccgaa gttactggcc tctatcttcc  
361 aggagaacca ggagccacag ccgcggctca cgcggccacccg caacattaag attacaagt  
421 gacacctgag tcagcaggac ctggaatccc agatgagaga gcttatctac acgactcaga  
481 tcttgttgc acccccattt tgacaatcc aaaggtgcag aaagcactct gacaattcca  
541 attgctaattc cagcatttgt ggatagctgc aaactgcgtt attgctgtatg agcgcttga  
601 cgccacattc cacactaacg tgggtgaa ttcttctggg cattgccagt acctgcctcc  
661 aggcatattc aagagttcct gtcacatcg

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## FIGURE 10

1 caggccgcca catagtccc gccaagtctt cggtgccctt tgccatttc cagccgcgt  
61 cccacgaggg tcacggcggc ggggagaggt ggagccgcga gagetcggcc gggggccccc  
121 cctggggcc gcggccatga cagcggctcg ggactggctc ctttccgcg cccctccgc  
181 cggagggtgag ggaagatgt ccatgtcagg gttcaaggcc aaaccgaagt tactggcctc  
241 tatctccag gagaaccagg agccacagcc gcggctcacg ccccacggca acattaagat  
301 tacaagtggc caccgtgagtc agcaggaccc ggaatcccag atgagagagc ttatctacac  
361 gactcagatc ttgttgtcac ccccattttt gacaatccaa aggtgcagaa agcactctga  
421 caaataatga aacaaccacc atcggttaaa ttgtatgcaa aaatattgca tctaccagca  
481 tttcagttc caattgctaa tccagcattt gtggatagct gcaaactgctg atattgctga  
541 tgagcgcctt gacgccccat tccacactaa cgtgtggtg aattctctg ggcattgcca  
601 gtacctgcct ccaggcatat tcaagagttc ctgctacatc g